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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 30, 2002, 12:32:18 ; Search time 10 Seconds (without alignments) 2086.259 Million cell updates/sec Run on:

US-10-025-514-8
2675
1 MSGKSFKAGVCPPKKSAQCL.....IEQNTKSPLFMGKVVNPTQK 503 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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MEDLINE-20386633; PubMed-10933492;
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Ellott p.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
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Human alpha 1-proteinos, molecular model and preliminary analysis
of the implications for function.";
J. Mol. Biol. 177:531-556(1984).
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Kurachi K., Chandra T., Friezner Degen S.J., White T.T.,
Marchloro T.L., Woo S.L.C., Davie E.W.;
"Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
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Laurell C.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The S variant of human alpha 1-antitrypsin, structure and implications for function and metabolism.";
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MEDLINE-82220035; PubMed-6979715;
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MEDLINE-85225507; PubMed=3873938;
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MEDLINE-82220135; PubMed-7045697;
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                                                                                                                                                                                                                                                             Nature 298:329-334(1982)
                                  rissue=Fetal liver;
                  SEQUENCE FROM N.A.
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"Molecular analysis of the gene of the alpha 1-antitrypsin deficiency
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antitrypsin normal M2 allele.";
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                                                                                                                                                                                                                                                                                                                                                                                                         "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
                                                                                                                                                                                                                                                                                                                                                                   Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F., Kalsheker N.A.;
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MEDLINE-90097863; Pubmed=1967187;
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                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90368097; PubMed=2394452;
                          MEDLINE=89352843; PubMed=2669992;
                                                                                                                                           MEDLINE=91315455; PubMed=1859394;
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                                                                                          Biosci. Rep. 9:129-138(1989)
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                                                Kalsheker N.;
                                                                              the gene.";
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                                                          96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTENKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                   216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                            276 GKIVDLVKELDRDTVFALNNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
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                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1-antitrypsin_precursor (Alpha-1 protease inhibitor) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-82082539; PubMed-7031661;
MEDLINE-82082539; PubMed-7031661;
Merachi K., Chandra T., Friezner Degen S.J., White T.T.,
Marchioro T.L., Moo S.L.C., Davie E.W.;
"Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
-I- FUNCTION: INHIBITOR OF SERINE PROTENSES. ITS PRIMARY TARGET IS
ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                       3;
      DB 1; Length 418;
                                   4; Indels
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97.8%; Pred. No. 5.7e-130;
tive 2; Mismatches 4;
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-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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             Best Local Similarity 97.8 Matches 399; Conservative
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Query Match
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96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
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                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and assignment to chromosome 7q2.4-q2.6.";
Anim. Genet. 27:85-89(1996).
-I- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                 Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal...
NON_TER 1 15
SIGNAL <1 15
                                                                                                                         374 REACTIVE BOND.
61 N-LINKED (GLCNAC. .) (POTENTIAL)
98 N-LINKED (GLCNAC. .) (POTENTIAL)
136 N-LINKED (GLCNAC. .) (POTENTIAL)
262 N-LINKED (GLCNAC. .) (POTENTIAL)
45694 MW; E19BOB7450FDBA9B CRC64;
                                                                                                                                                                                                                        DB 1; Length 409;
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                                                                                                                                                                                                                                   90.2%; Pred. No. 2e-120; ive 21; Mismatches 1
                                                                                                                                                                                                                        71.4%; Score 1909.5;
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MEDLINE=97009792; PubMed=8856896;
             InterPro; IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                               368; Conservative
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98
136
262
409 AA;
 HSSP; P01009; 9API,
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                                                                                                                        ACT_SITE
CARBOHYD
                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                     Local
                                                                                                            CHAIN
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NCBI_TaxID=64664;
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CARBOHYD
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CARBOHYD
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 ASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 LGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 LGMFDLHHCDKLSSWVLLMDYVATATAFFILPDQGKLHQLEDMLTKEIRAKFLEKRYPSS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 NQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 GTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQD---HPTFNKITPNLAEFAFSLYRQLAH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 QSNSTWIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Callosciurus caniceps (Gray-bellied squirrel).
Callosciurus caniceps (Gray-bellied squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
       ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                                                                                                                                                                                                                                                                                                          REACTIVE BOND.
N-LINKED (GECNAC. .) (POTENTIAL).
N-LINKED (GECNAC. .) (POTENTIAL).
0844AB2A9E600690 CRC64;
                                                                                                                                                                                                                                                                                          Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal. SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 GTERAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFWGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                69; Indels
                                                                                                                                                                                                                                                                                                                            ALPHA-1-ANTITRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                Match 56.4%; Score 1508; DB 1; Local Similarity 72.0%; Pred. No. 1.3e-93; les 296; Conservative 40; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 AA.
                              THROMBIN (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Extracellular.
--- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                        421 AA; 47194 MW;
                                                                                                                                                                                                                         HSSP; P01009; 9API.
InterPro; IPR000215; Serpin.
                                                                                                                                                                                                        EMBL; X88780; CAA61259.1; -.
                                                                                                                                                                                                                                                      Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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054763;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDXVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 18; Score 1500; DB 1; Length 412; 71.08; Pred. No. 4.4e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Indels
                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUE SPECIFICITY: PLASMA.
-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 412 AL
377 378 RE
65 65 N-
102 102 N-
165 165 N-
266 266 N-
412 AA; 45729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB000552; BAA24422.1; -.
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InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 71.0%
Matches 289; Conservative
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chao S., Chai K.X., Chao L., Chao J.; "Molecular cloning and primary structure of rat alpha 1-antitrypsin."; Blochemistry 29:323-329(1990).
                                                                                                                                                                                                                                                                                                                               Misumi Y., Sohda M., Ohkubo K., Takami N., Oda K., Ikehara Y., "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease inhibitor and its expression in COS-1 cells.";
                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                Filink I.L., Balley T., Morkin E.;
Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
•!- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                        01-FEB-1991 (Rel. 17, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> G (IN REF. 2).
L -> V (IN REF. 2).
M -> I (IN REF. 3).
H -> Y (IN REF. 2).
K -> M (IN REF. 2).
S -> D (IN REF. 3).
W; B4245CFE21C5C761 CRC64;
                                                                                                                                                                                     SEQUENCE OF 4-411 FROM N.A., AND SEQUENCE OF 25-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA-1-ANTIPROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- TISSUE SPECIFICITY: PLASMA.
                     411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REACTIVE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                              MEDLINE-90148955; PubMed-2302382;
                                                                                                                                                                                                                                                                                                     STRAIN-Wistar; TISSUE-Liver;
MEDLINE-91035351; Pubmed-2229024;
                                            01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 188-389 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M32247; AAA40788.1; --
EMBL; D00675; BAA06579.1; --
EMBL; X16273; CAA34349.1; --
PIR; A33892; ITRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377
64
101
265
                                                                                                  proteinase inhibitor
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
             AlAT_RAT
P17475;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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A1AT_RAT
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DB 1; Length 411;

Score 1467.5; DB] Pred. No. 6.5e-91;

54.9%; 67.1%;

Best Local Similarity

Query Match

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                         89 RDLKCCMGMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKTTPNLAEFAFSLYR 148
                                                                                149 QLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQEL 208
                                                                                                209 LRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQIND 268
                                                                                                                                                         269 YVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVP 328
                                                                                                                                                                                                               329 MMKRLGMFNIOHCKKLSSWVLLMKYLGNATALFFLPDEGKLQHLENELTHDITTKFLENE 388
                                                                                                                                                                                                                                                                                                           389 DRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLT 448
        Gaps
                                                                                                                                                                                                                                                                      MEDLINE-89366677; PubMed=2788872;
Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.;
"Nucleotide and deduced amino acid sequence of sheep alpha 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
     .;6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1989 (Rel. 12, Last sequence update)
01-0cT-1994 (Rel. 30, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                  449 IDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                    Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.; "Isolation and characterization of sheep alpha 1-proteinase
       61; Indels
Matches 278; Conservative 66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 17:6398-6398(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91144555; PubMed-1899999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteinase inhibitor).
Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 25-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlAT_SHEEP
P12725;
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Indels
                                                                                                                                                                                                                                                                                             Serpin; Serine protease inhibitor; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 FLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ||| :||::||::||::|| 371 FLEMIPMALPPDWKFDRPFLVVIYEHHTKSPLFVGKVVNPT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%; Score 1447.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Mismatches
                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                  EMBL; AB000546; BAA24416.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             46212 MW;
                                                                                                                                                                                                                                           InterPro; IPR000115; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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25
65
102
165
266
378
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                                                                                ANTITRYPSIN.
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P34955;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 YVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVP 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-1-antirrypsin-like protein CM5-MM precursor.
Aramias sibiricus (Sibberian chipmunk) (Asian chipmunk).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 IDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                           Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
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                                                                                                                                                                                                                                                                                                             DB 1; Length 416;
                                                                                                                                                                                                                                                                                                                                        67; Indels
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Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
                                                                                                                                                                                                                                                      A -> S (IN REF. 2).
C -> A (IN REF. 2).
0B4702C0527321BF CRC64;
                                                                                                                                                                         ALPHA-1-ANTIPROTEINASE
                                                                                                                                                                                                                                                                                                               54.8%; Score 1465.5; DB 67.6%; Pred. No. 8.9e-91;
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                                                                                                                                                                                                                                                                                                                                            62; Mismatches
                                                                                                                                                                                          REACTIVE BOND
                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                       45984 MW;
                                                                                          InterPro; IPR000215; Serpin.
                                                   EMBL; X15555; CAA33561.1; -. PIR; S05312; ITSH.
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                                                                                                                                  PROSITE; PS00284; SERPIN;
                                                                                                         Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1
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68
105
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68
105
143
269
39
45
416 AA;
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                                                                                HSSP; P01009; 1KCT
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054757;
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CARBOHYD
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ALMM_TAMSI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-priofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXXLIC ALID (POTENTIAL).
PYRROLIDONE CARBOXXLIC ALID (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 SITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAM 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKL 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 LTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 LVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQH 340
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413 AA;
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054759:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 RGLLLLAALC---CLAPISLAGVLQGHAVQETDDTSHQE--AACHKIAPNLANFAFSIYH 61
                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.1%; Score 1447.5; DB 1; Length 416;
                                                                                                                      Sinha D., Bakhshi M.R., Kirby E.P.,
"Complete CDNA sequence of bovine alpha 1-antitrypsin.";
Blochim. Biophys. Acta 110:209-212(1992).
-!- SUBCELCLIAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: PLASMA.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
ALPHA-1-ANTIPROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.4e-89; 62; Mismatches 70
                                                                                                          MEDLINE-92223096; PubMed-1562597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46104 MW;
                                                                                                                                                                                                                                                                                      EMBL; X63129; CAA44840.1; -. PIR; S21097; S21097. PIR; S18920; S18920.
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InterPro; IPR000115; Serpin.
Pfam; PF00079; SerPin; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 277; Conservative
                                                     Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
   proteinase inhibitor).
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                                                                                      SEQUENCE FROM N.A.
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PYRROLIDONE CARBOXYLLC ACID (POTENTIAL).
N-LIKED (GLCNAC. .) (POTENTIAL).
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C., Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.; Expression of multiple alphal antitrypsin-like genes in hibernating Species of the squirrel family."; Gene 204:127-132(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 SCLGPGSLAQD----AQETEASKQDQEHPASHRIAPHLAEFALSFYRVLARQSNTTNIF 70
                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-1-antitrypsin-like protein CM55-ST precursor.
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
-!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-ANTITRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serpin; Serine protease inhibitor; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 1403.5; DB
66.5%; Pred. No. 1.2e-86;
ive 61; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98094263; Pubmed=9434174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB000548; BAA24418.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.58
Matches 268; Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00284; SERPIN;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                          ALMS_TAMSI
054758:
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-SI.
PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 SCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIF 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SCLGPGSLAQD-----AQETEASKQDQEHPASHKIAPHLAEFALSFYRVLARQSNTTNIF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;

MEDLINE-980453; PubMed-9434174;

MEDLINE-980453; PubMed-9434174;

Takamatsu N., Kojima M., Tanlyama M., Obba K., Uematsu T., Segawa C., Takamatsu N., Kojima M., Tanlyama M., Kondo J., Kondo N., Shiba T.;

Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;

"Expression of multiple alphal-antitrypsin-like genes in hibernating species of the squirrel family.";

Species of the squirrel family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                          251 CSTLASWVLQMDYLGNATAIFLLPDKGKMQHLEDTVTTEILTKFLKNRQTTKSQLYFPKV 310
                                                                                  401 SITGTYDLKSVLGQLGITKVFSNGADLSGYTEEAPLKLSKAVHKAVLTIDEKGTEAAGAM 460
                                                                                                 191 LLKELDRDTVLALVNYIFFKGKWKQPFNEEQTREKDFHVDEATTVRVPMMNRLGMFHLHH 250
                           341 CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKL 400
                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-1-antitrypsin-11ke protein CM55-51 precursor.
Taminas Sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 204:127-132(1997).
-!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serpin; Serine protease inhibitor; Glycoprotein; Signal. SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB65AlD31B8CA2EC CRC64;
                                                                                                                                           461 FLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                          371 VLGNIRSTLRYEVIFDRPFLVVIYEHHTKSPLFVGKVVNPTQQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 2.3e-86; 61; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.3%; Score 1399.5;
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HSSP; P01009; 9API.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46202 MW;
                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268; Conservative
                                                                                                                                                                                                                                                 STANDARD;
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25
65
102
165
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165
266
377
413 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=64680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTITRYPSIN.
                                                                                                                                                                                                                                                ALSI_TAMSI
054760:
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
PLINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 SITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAM 460
                                                                                                                                                                                                                                                                                                                                                                                                         281 LVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQH 340
                                                                                                                                                                                                                   341 CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKL 400
                        LTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVD 280
                                                                                                                       161 FSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-1-antitrypsin-like protein CM55-MS precursor.
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostoml;
Mammalia, Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serpin; Serine protease inhibitor; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 FLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=98094263; PubMed=9434174;
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InterPro; IPR000215; Serpin.
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                                                                                                                101 SCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIF 160
                                                                                                                                                                          161 FSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQ 220
                                                                                                                                                                                                                                     221 LTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVD 280
                                                                                                                                                                                                                                                    LVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQH 340
                                                                                                                                                                                                                                                                                                               341 CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKL 400
                                                                                                                                     401 SITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAM 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 211-413 FROM N.A.
MEDLINE-86163765; PubMed-3007061;
Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;
"Isolation and characterization of the alpha 1-antitrypsin gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA 5:29-36(1986).
-1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
266 266 N-LINKED (GLCNAC. . ) (POTENTIAL).
377 378 REACTIVE BOND (BY SIMILARITY).
413 AA; 45952 MW; 430374CA26EBAF08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1-antirypsin 1-1 precursor (Serine protease inhibitor 1-1)
(Alpha-1 protease inhibitor 1) (Alpha-1-antiproteinase) (AAT).
                                                                 DB 1; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borriello F., Krauter K.S.; "Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence.";
                                                         51.9%; Score 1387.5; DB 1; Length 67.0%; Pred. No. 1.4e-85; Live 55; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 FLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Liver; MEDLINE-92052104; PubMed-1946354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
                                                                                  Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1T1_MOUSE
P07758;
              ACT_SITE
SEQUENCE
CARBOHYD
                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1347,
Pred. No. 7.3e-83;
Limmatches 72; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GLC---CLVPSFLAED-----VQETDTSQKDQS-PASHEIATNLGDFAISLYRELVHQSN 64
                                                                                                                                                                                                                                                                            ALPHA-1-ANTITRYPSIN 1-1.
REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                              PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIT2_MOUSE STANDARD; PRT; 413 AA. P2259; 061283; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2011 (Rel. 40, Last annotation update) 18-Danitarypsin 1-2 precursor (Serine protease inhibitor 1-2) (Alpha-1 protease inhibitor 2) (Alpha-1 antiproteinase) (AAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 H -> D (IN REF. 2).
323 P -> L (IN REF. 2).
4004 L -> V (IN REF. 2).
46002 MW; 1124B2CC356232F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       50.4%; Score 1347; DB 1;
                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.3%; Prea. ...
tive 72; Mismatches
European Bioinformatics Institute.
                                                                                       EMBL; M75721; AAC28869.1; -.
EMBL; M12586; AA51624.1; -.
PIR; A25495; A25495.
                                                                                                                                     HSSP; P01009; BAPI.
MGD; MGI:891971; Spil-1.
InterPro; IPR0002115; Serpin.
Pfam; PFC0079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 62.3% Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        413 AA;
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                                                                                                                                                                                                                                                Multigene family.
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CARBOHYD
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336 FNIQHCKKLSSWYLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                          A1T3_MOUSE
Q00896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
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ALPHA-1-ANTITRYPSIN 1-2.

REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                              Sifers R.N., Ledley F.D., Reed-Fourquet L., Ledbetter D.H., Ledbetter S.A., Woo S.L.C.; "Complete cDNA sequence and chromosomal localization of mouse alpha
                                                                                                                                                                                                                                                     evolutionary divergence.";

Proc. natl. Acad. Sci. U.S.A. 88:9417-9421(1991).

Proc. natl. Acad. Sci. U.S.A. 88:9417-9421(1991).

Proc. INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS

ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
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                                                                                                                                                                                         STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-92052104; PubMed-1946354;
Borriello F., Krauter K.S.;
"Multiple murine alpha 1-protease inhibitor genes show unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%; Score 1345; DB 1; Length 413; 62.6%; Pred. No. 9.9e-83;
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G -> A (IN REF. 2).

T -> M (IN REF. 2).

T -> I (IN REF. 2).

E -> D (IN REF. 2).

E -> D (IN REF. 2).

W, D93B7BB04E9446BC CRC64;
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                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                            SEQUENCE FROM N.A.
MEDLINE=90152670; PubMed=2303252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:891970, Spil-2.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin: 1
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                                                                                                                                                                                 SEQUENCE OF 12-413 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00284; SERPIN;
                                                                                                                                                    Senomics 6:100-104(1990).
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314 3
413 AA;
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265
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CARBOHYD
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                                                                      396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                 245 LDVHHCSTLSSWYLLMDYAGNASAVFLLPEDGKMQHLEGTLNKELISKILLNRRRRLVQI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92052104; PubMed=1946354;
MEDLINE=92052104; PubMed=1946354;
Borriello F., Krauter K.S.;
"Multiple murine alpha 1-protease inhibitor genes show unusual
"Multiple murine alpha 1-protease inhibitor genes show unusual
evolutionary divergence.",
Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                             15.-UUL-1998 (Rel. 36, Created)
15.-UUL-1998 (Rel. 36, Last sequence update)
16.-CUT-2001 (Rel. 40, Last annotation update)
Alpha-1-antitypsin 1.3 precursor (Serine protease inhibitor 1-3)
(Alpha-1 protease inhibitor 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
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REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                              455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEONTKSPLFWGKVVNPTOK 503
                                                                                                                                                                                                      7EAD710919EA1C5B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                       413 AA.
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Matches 256; Conservative
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InterPro; IPR000215; Serf
Pfam; PF00079; serpin; 1.
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413
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156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                    DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                            276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                          336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                  396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-41.
MEDLINE-88227895; PubMed-3259574;
Salto A., Sinohara H.;
"Differential interactions of rabbit plasma alpha-1-antiproteinases and F with portine trypsin.";
"Blochem. 103:247-253(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Alpha-1-antiproteinase F precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor) (APF)
Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiproteinases.";
J. Biochem. 108:80-85(1990).
-!- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Clouing and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F: amino acid sequence comparison of alpha-1-antiproteinases of six mammals.";
J. Blochem. 109:158-162(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salto A., Sinohara H.;
"Amino acid sequence at the reactive site of rabbit alpha-1-
                                                                                                                                                                                                                                                                                                                     455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                           -i- TISSUE SPECIFICTTY: PLASMA.
-i- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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MEDLINE-91035333; PubMed-2229014;
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Saito A., Sinohara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9986;
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P23035;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           217 SQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMF 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 NIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLH 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 LPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 378 REACTIVE BOND.
65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
230 N-LINKED (GLCNAC. .) (POTENTIAL).
266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
413 AA; 45867 MW; E851F5DE63A592DF CRC64;
                                                                                                                                          Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal
                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                             DB 1; Length 413;
                                                                                                                                                                                                                                                                                                    82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA-1-ANTIPROTEINASE F.
                                                                                                                                                                                                                                                                          Score 1339.5; DB Pred. No. 2.3e-82
                                                                                                                                                                                                                                                                                                   64; Mismatches
                                   EMBL; X57710; CAA40881.1; --
EMBL; D00853; BAA00728.1; --
PIR; JX0154, JX0154.
HSSP; P01009; BAPI.
InterPro; IPR000215; Serpin.
Pfam; PF00079; Serpin.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                   62.8%;
                                                                                                                            PROSITE; PS00284; SERPIN; 1
                                                                                                                                                                                                                                                                                                 Matches 255; Conservative
                                                                                                                                                                     413
378
65
102
230
266
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                ACT_SITE
CARBOHYD
                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                         SIGNAL
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